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Title : Phylogeography and population genetic structure of the Southeast Asian dugong (Dugong dugon), Thailand: Implications for conservation.

Category : Conservation

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Abstract : In the order Sirenia, there are only three extant species of manatees and the dugong. The dugong (*Dugong dugon*) is listed as “vulnerable” to extinction by the IUCN. Of particular concern in the present study is the Southeast Asian dugong population of Thailand, which is considered an endangered marine mammal in Thai waters. There is little known about the populations along the east (Gulf of Thailand) and west (Andaman) coasts of Thailand, not even total population size. It is therefore apparent that there is an extreme need for research to be conducted to assess the current status of the dugongs in Thailand. In this study, the population genetic structure and phylogeography of the Southeast Asian dugong in Thailand was assessed through the use of mitochondrial DNA control region sequencing. Twelve haplotypes were identified among 45 dugongs from the Andaman Sea and the Gulf of Thailand. Sequence variation analysis revealed a high degree of nucleotide diversity ($d=6.48\%$) for the entire dugong population of Thailand. Phylogenetic analysis revealed that each of the twelve haplotypes identified occurred in both the Andaman Sea and Gulf of Thailand populations. This indicates the likelihood of gene flow between these two populations since the end of Pleistocene. During this time no geographic or oceanographic barriers existed along the Malacca Strait, thus ensuring a stable migration corridor between the Andaman Sea and Gulf of Thailand. The results of this study have also identified eight genetically distinct subpopulations along the coastline of Thailand. Therefore, we suggest that three reserves (a northeast reserve extending from Chon Buri to Rayong; a mid-east reserve at Surat Thani; and a southwest reserve ranging from Phuket to Trang) be established along the Thailand coastline to ensure the preservation of the majority (seven) of these threatened and genetically unique subpopulations.